AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1. (Original) A positionally addressable array comprising a substrate to which are attached a plurality of different biopolymer probes, said different biopolymer probes in said plurality being situated at different positions on said surface and being the product of a step-by-step synthesis of said biopolymer probes on said substrate, said plurality of different binding probes comprising a plurality of quality control probes, each quality control probe in said plurality comprising (i) the same predetermined binding sequence or (ii) a different predetermined binding sequence with the same binding specificity, the synthesis of said predetermined binding sequence in each said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis.

2. (Original) The array of claim 1 wherein the sequence of each said quality control probe of said plurality consists of said predetermined binding sequence.

3. (Original) The array of claim 1 wherein said plurality of quality control probes comprise a second sequence consisting of a chemical structure contiguous with said predetermined binding sequence, wherein at least some of said quality control probes differ from other of said quality control probes in the length of said chemical structure.

4. (Original) The array of claim 3 wherein said chemical structure is a sequence of number 0 to N monomers contiguous with said predetermined binding sequence, and where N is a whole number equal to or greater than 1.

5. (Original) A method of determining if a positionally-addressable biopolymer array has a synthesis defect comprising the following steps in the order stated:

a) contacting the array of any of claims 1-2 with a sample comprising a binding partner that binds said predetermined binding sequence;

b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes, wherein if said binding is similar, the absence of a synthesis defect between said sequential cycles of synthesis of said array is indicated.

6. (Original) A method of determining if a positionally-addressable biopolymer array has a synthesis defect comprising the following steps in the order stated:

a) contacting the array of claim 3 with a sample comprising a binding partner that binds said predetermined binding sequence;

b) detecting or measuring binding between (i) two or more of said quality control probes that differ in the number of said monomers; and (ii) said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes; wherein if said binding is similar, the absence of a synthesis defect between said sequential cycles of synthesis used to synthesize said two or more quality probes is indicated.

7. (Original) The method of claim 5 wherein said comparing comprises determining the binding ratio of two of said two or more quality control probes, wherein said binding ratio is the amount of binding of a first of said two quality control probes with said binding partner, divided by the amount of binding of a second of said two quality control probes with said binding partner, and wherein said binding ratio between 0.5 and 2.0 indicates the absence of said synthesis defect.

8. (Original) The method of claim 6 wherein said comparing comprises determining the binding ratio of two of said two or more quality control probes, wherein said binding ratio is the amount of binding of a first of said two quality control probes with said binding partner, divided by the amount of binding of a second of said two quality control probes with said binding partner, and wherein said binding ratio between 0.5 and 2.0 indicates the absence of said synthesis defect.

9. (Currently Amended) The method of claim [[5 or]] 6 further comprising before step (a) the step of synthesizing said array.

10. (Currently Amended) The method of claim [[5 or]] 6 wherein said sample comprises (i) total cellular RNA or mRNA from one or more cells or a plurality of nucleic acids derived therefrom, and (ii) said binding partner, wherein said binding partner is not expressed by said cells.

11. (Original) The array of claim 2, 3, or 4 wherein said biopolymer probes are nucleic acids.

12. (Original) The array of claim 11 wherein said predetermined binding sequence is in the range of 10-40 nucleotides in length.

13. (Original) The array of claim 11 wherein said biopolymer probes consist of a sequence in the range of 20-100 nucleotides.

14. (Original) The array of claim 12 wherein said predetermined binding sequence is 25 nucleotides in length.

15. (Original) The array of claim 14 wherein said predetermined binding sequence is SEQ ID NO:1 or a complement thereof.

16. (Original) The array of claim 2, 3, or 4 wherein said biopolymer probes are proteins.

17. (Original) The array of claim 16 wherein said proteins are antibodies.

18. (Original) The array of claim 2 wherein said predetermined binding sequence of said quality control biopolymer probe is between 10-75% of the length of the length of the biopolymer probes on the array that are not said quality control probes.

19. (Original) The array of claim 18 wherein said predetermined binding sequence consists of 25 monomers, and wherein said biopolymer probes on the array that are not said quality control probes consist of 60 monomers.

20. (Original) The array of claim 4 wherein N is not greater than the number of monomers in said biopolymer probes on the array that are not said quality control biopolymer probes minus the number of monomers in said predetermined binding sequence.

21. (Original) The array of claim 4 wherein N is greater than the number of monomers in said biopolymer probes on the array that are not said quality control biopolymer probes minus the number of monomers in said predetermined binding sequence.

22. (Original) The array of claim 4 which comprises three of said quality control probes that differ in N.

23. (Original) The array of claim 22 wherein N is 0, 20, and 35, respectively, for different quality control probes.

24. (Original) A method of making a positionally-addressable array of a plurality of different biopolymer probes comprising synthesizing said plurality of different biopolymer probes on a substrate from monomers using a step-by-step synthesis such that each of said different biopolymer probes is attached to said substrate at a different position on said substrate, wherein said plurality of different biopolymer probes comprise a plurality of quality control probes, each quality control probe in said plurality comprising the same predetermined binding sequence, wherein the synthesis of said predetermined binding sequence in each of said quality control probes is initiated during said step-by-step synthesis at sequential cycles of synthesis.

25. (Original) The method of claim 24 wherein the sequence of each said quality control probe of said plurality consists of said predetermined binding sequence.

26. (Original) The method of claim 24 wherein said plurality of quality control probes comprise a second sequence of number 0 to N monomers contiguous with said predetermined binding sequence, wherein at least some of said quality control probes differ from other of said quality control probes in the number of said monomers, and where N is a whole number equal to or greater than 1.

27. (Original) The array of claim 1 wherein said plurality of quality control probes comprise

(i) quality control probes whose sequence consists of said predetermined sequence; and

(ii) quality control probes that comprise a second sequence of number 0 to N monomers contiguous with said predetermined binding sequence, wherein at least some of

said quality control probes differ from other of said quality control probes in the number of said monomers, and where N is a whole number equal to or greater than 1.

28. (Original) The array of claim 27 wherein said biopolymer probes are oligonucleotides, said predetermined sequence consists of 25 nucleotides, and said biopolymer probes that are not said quality control probes consist of 60 nucleotides.

29. (Original) An oligonucleotide comprising a nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:2 or the complement thereof.

30. (Original) A positionally addressable array comprising a substrate to which are attached a plurality of different biopolymer probes, said different biopolymer probes in said plurality being situated at different positions on said surface and being the product of a step-by-step addition of monomers to said biopolymer probes on said substrate, said plurality of different biopolymer probes comprising a plurality of quality control probes, each quality control probe in said plurality comprising at least one labeled monomer, the addition of said labeled monomer to said quality control probe having been initiated during said step-by-step synthesis at sequential cycles of synthesis.

31. (Original) A method of determining if the positionally-addressable biopolymer array of claim 30 has a synthesis defect comprising comparing the signal from said at least one labeled monomer of two or more of said quality control probes, wherein if said signal is similar, the absence of a synthesis defect between said sequential cycles of synthesis of said array is indicated.

32. (Original) The method of claim 31 wherein said comparing comprises determining the signal ratio of two of said two or more quality control probes, wherein said signal ratio is the amount of signal emitted from a first of said two quality control probes divided by the amount of signal emitted from a second of said two quality control probes, and wherein said signal ratio between 0.5 and 2.0 indicates the absence of said synthesis defect.

33. (Original) The array of claim 30 wherein said biopolymer probes are nucleic acids.

34. (Original) The array of claim 33 wherein said biopolymer probes consist of a sequence in the range of 20-100 nucleotides.

35. (Original) The array of claim 30 wherein said biopolymer probes are proteins.

36. (Original) The array of claim 35 wherein said proteins are antibodies.

37. (Currently Amended) The method of any one of claims [[5,]] 6[[,]] and 31 wherein said synthesis defect is a nozzle failure.

38. (Original) The method of claim 37 wherein said array comprises at least a portion of said quality control probes arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, and where P is a whole number equal to or greater than 1.

39. (Original) The method of claim 38 wherein P equals 20.

40. (Original) A method of detecting a nozzle failure using the positionally addressable array of claim 1 or 2 comprising the following steps in the order stated:

a) contacting the array of any of claims 1 or 2 with a sample comprising a binding partner that binds said predetermined binding sequence, wherein at least a portion of said plurality of quality control probes is arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, wherein P is a whole number equal to or greater than 1;

b) detecting or measuring binding between two or more of said quality control probes and said binding partner in the sample; and

c) comparing binding of said two or more of said quality control probes in a periodicity of P, wherein if said binding is similar, the absence of a nozzle defect is indicated.

41. (Original) A method of detecting a nozzle failure using the positionally addressable array of claim 30 comprising comparing the signal from said at least one labeled monomer of two or more of said quality control probes in a periodicity of P, wherein at least

a portion of said plurality of quality control probes is arranged in a periodicity of P and wherein said array is synthesized by a step-by-step synthesis using an inkjet printhead with P nozzles, wherein if said signal is similar, the absence of a nozzle defect is indicated, and wherein P is a whole number equal to or greater than 1.

42. (New) The method of claim 5 further comprising before step (a) the step of synthesizing said array.

43. (New) The method of claim 5 wherein said sample comprises (i) total cellular RNA or mRNA from one or more cells or a plurality of nucleic acids derived therefrom, and (ii) said binding partner, wherein said binding partner is not expressed by said cells.

44. (New) The method of claim 5 wherein said synthesis defect is a nozzle failure.

45. (New) The method of claim 44 wherein said array comprises at least a portion of said quality control probes arranged in a periodicity of P and wherein said array is synthesized by step-by-step synthesis using an inkjet printhead with P nozzles, and where P is a whole number equal to or greater than 1.

46. (New) The method of claim 45 wherein P equals 20.